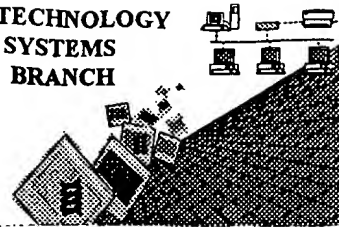*E. Slobodyansky*

RAW SEQUENCE LISTING
ERROR REPORT

17

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/830,111 B

Source: 1600

Date Processed by STIC: 6/5/2003

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
> http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
   > Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 09/830,111B |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____Variable Length

Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____Skipped Sequences
(OLD RULES)

Sequence(s)____missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences
(NEW RULES)

Sequence(s)____missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10____Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____Use of <220>

Sequence(s) 3-8 missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

Sequence listing

<110> Kaneka Corporation

<120> Process for producing coenzyme Q10

<130> T549/QX-GT2

<150> JP P1999-237561
<151> 1999-08-24

<160> 28   *8 do not use underlines*
         delete Z

Does Not Comply
Corrected Diskette Needed

see pp 1, 4-5

#17

<210> 1
<211> 1653
<212> DNA
<213> Saioella complicata

<400> 1

```
ttttgtggggg tcgaaaagtc ggcacgggtg caggttcggc ttgagaccag taaaggctcg   60

gagattgagt tcaggacaaa gctttgatcc gtgaggtcta catcttcagc aaatcatttc  120

aaatccatat acc atg gcc tca cca gca ctg cgg ata cga agc atc agc     169
            Met Ala Ser Pro Ala Leu Arg Ile Arg Ser Ile Ser
             1           5              10

tct cga tca atc gcc tct ctg cga tcg gtt acc cta aga aca gcc tcg   217
Ser Arg Ser Ile Ala Ser Leu Arg Ser Val Thr Leu Arg Thr Ala Ser
         15              20              25

gca cct tca tta cga cta aga tgt acc ccg acg agc cgg cca tcg agt   265
Ala Pro Ser Leu Arg Leu Arg Cys Thr Pro Thr Ser Arg Pro Ser Ser
     30          35                  40

tca tgg gct gct gct gtg tct tcg gcg tcg aga ctg gtt gag cct gat   313
Ser Trp Ala Ala Ala Val Ser Ser Ala Ser Arg Leu Val Glu Pro Asp
 45              50              55              60

ccg aat caa cct ctc atc aat ccg ctc aac ttg gtc ggt ccc gag atg   361
Pro Asn Gln Pro Leu Ile Asn Pro Leu Asn Leu Val Gly Pro Glu Met
                 65              70              75

tca aat ctt aca tcc aac atc cga tct ctc ctc ggt tca gga cac cct   409
Ser Asn Leu Thr Ser Asn Ile Arg Ser Leu Leu Gly Ser Gly His Pro
             80              85              90

tct ctc gac act gtc gct aaa tac tat gtt cag tct gag gga aag cat   457
Ser Leu Asp Thr Val Ala Lys Tyr Tyr Val Gln Ser Glu Gly Lys His
         95              100             105

att cgt ccg ctc atg gta ctg ctg atg gct cag gcg acg gag gtt gcg   505
Ile Arg Pro Leu Met Val Leu Leu Met Ala Gln Ala Thr Glu Val Ala
 110             115             120

cca aaa gtt cag ggt tgg gag aag gtc gtg gag gtt ccg gtg aac gag   553
Pro Lys Val Gln Gly Trp Glu Lys Val Val Glu Val Pro Val Asn Glu
125             130             135             140
```

```
gga ctc gca cca cca gag gtg ctc aat gac aag aac cca gat atg atg    601
Gly Leu Ala Pro Pro Glu Val Leu Asn Asp Lys Asn Pro Asp Met Met
            145                     150                 155

aac atg agg tca gga cca tta acg aag gac ggc gag atc gag gga cag    649
Asn Met Arg Ser Gly Pro Leu Thr Lys Asp Gly Glu Ile Glu Gly Gln
            160                 165                 170

acg tcg aat atc ctc gcc tcg caa cgg cgg ttg get gag atc acg gag    697
Thr Ser Asn Ile Leu Ala Ser Gln Arg Arg Leu Ala Glu Ile Thr Glu
            175                 180                 185

atg atc cat gca gca tca ctc ctc cac gac gac gtt atc gac get tcc    745
Met Ile His Ala Ala Ser Leu Leu His Asp Asp Val Ile Asp Ala Ser
        190                 195                 200

gag acc aga cga aac gca cca tcc gga aac cag gca ttc gga aac aag    793
Glu Thr Arg Arg Asn Ala Pro Ser Gly Asn Gln Ala Phe Gly Asn Lys
205                 210                 215                 220

atg gcg att ttg get ggt gat ttc ttg ttg gga cgg gcg tct gtt gca    841
Met Ala Ile Leu Ala Gly Asp Phe Leu Leu Gly Arg Ala Ser Val Ala
            225                 230                 235

ttg gcg agg ttg cgc aat ccg gag gtg att gag ctt ttg get act gtt    889
Leu Ala Arg Leu Arg Asn Pro Glu Val Ile Glu Leu Leu Ala Thr Val
            240                 245                 250

att gca aac ttg gtt gag gga gag ttc atg cag ttg aaa aat act gtt    937
Ile Ala Asn Leu Val Glu Gly Glu Phe Met Gln Leu Lys Asn Thr Val
        255                 260                 265

gat gat gcg att gag get acg gcg acg cag gaa acg ttc gat tac tat    985
Asp Asp Ala Ile Glu Ala Thr Ala Thr Gln Glu Thr Phe Asp Tyr Tyr
270                 275                 280

ttg cag aag act tac ttg aag act gcg tcc ttg att gcc aag tcg tgc   1033
Leu Gln Lys Thr Tyr Leu Lys Thr Ala Ser Leu Ile Ala Lys Ser Cys
285                 290                 295                 300

aga gca agt gcg ctt etg ggt ggt get acg ect gag gtt get gat get   1081
Arg Ala Ser Ala Leu Leu Gly Gly Ala Thr Pro Glu Val Ala Asp Ala
            305                 310                 315

gct tat gct tac gga agg aac ctt ggt ttg gca ttc cag atc gtc gac   1129
Ala Tyr Ala Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gln Ile Val Asp
            320                 325                 330

gac atg ctc gac tac acc gtc tcc get acc gac ctc ggt aag ccc gcc   1177
Asp Met Leu Asp Tyr Thr Val Ser Ala Thr Asp Leu Gly Lys Pro Ala
            335                 340                 345

ggt gca gac ctc cag ctc ggt ctc gcc acc gcg ccg gcc ctc ttc gca   1225
Gly Ala Asp Leu Gln Leu Gly Leu Ala Thr Ala Pro Ala Leu Phe Ala
            350                 355                 360

tgg aag cac cac gcc gag ctc ggt ccc atg atc aag cgc aag ttc tct   1273
Trp Lys His His Ala Glu Leu Gly Pro Met Ile Lys Arg Lys Phe Ser
365                 370                 375                 380
```

```
gac cca gga gac gtc gag cgt gca cgc gag ttg gtc gag aaa agt gat   1321
Asp Pro Gly Asp Val Glu Arg Ala Arg Glu Leu Val Glu Lys Ser Asp
             385                 390                 395

gga ttg gag aag acg aga gcc ttg gcg gag gag tat gcc cag aag gcg   1369
Gly Leu Glu Lys Thr Arg Ala Leu Ala Glu Glu Tyr Ala Gln Lys Ala
             400                 405                 410

ttg gat gca att cgg acg ttc ccg gag agt ccg gca cgg aag gct ttg   1417
Leu Asp Ala Ile Arg Thr Phe Pro Glu Ser Pro Ala Arg Lys Ala Leu
             415                 420                 425

gag cag ttg acg gac aag gtg ttg act agg tca aga taggaattcgagct   1467
Glu Gln Leu Thr Asp Lys Val Leu Thr Arg Ser Arg
         430                 435                 440

cggtacccgg ggatcctcta gagtcgacct gcaggcatgc aagcttggct gttttggcgg 1527

atgagagaag attttcagcc tgatacagat taaatcagaa cgcagaagcg gtctgataaa 1587

acagaatttg cctggcggca gtagcgcggt ggtcccacct gaccccatgc cgaactcaga 1647

agtgaa                                                             1653
```

```
<210> 2
<211> 440
<212> PRT
<213> Saioella complicata

<400> 2
Met Ala Ser Pro Ala Leu Arg Ile Arg Ser Ile Ser Ser Arg Ser
  1               5              10                  15
Ile Ala Ser Leu Arg Ser Val Thr Leu Arg Thr Ala Ser Ala Pro
             20                  25                  30
Ser Leu Arg Leu Arg Cys Thr Pro Thr Ser Arg Pro Ser Ser Ser
             35                  40                  45
Trp Ala Ala Ala Val Ser Ser Ala Ser Arg Leu Val Glu Pro Asp
             50                  55                  60
Pro Asn Gln Pro Leu Ile Asn Pro Leu Asn Leu Val Gly Pro Glu
             65                  70                  75
Met Ser Asn Leu Thr Ser Asn Ile Arg Ser Leu Leu Gly Ser Gly
             80                  85                  90
His Pro Ser Leu Asp Thr Val Ala Lys Tyr Tyr Val Gln Ser Glu
             95                 100                 105
Gly Lys His Ile Arg Pro Leu Met Val Leu Leu Met Ala Gln Ala
            110                 115                 120
Thr Glu Val Ala Pro Lys Val Gln Gly Trp Glu Lys Val Val Glu
            125                 130                 135
Val Pro Val Asn Glu Gly Leu Ala Pro Pro Glu Val Leu Asn Asp
            140                 145                 150
Lys Asn Pro Asp Met Met Asn Met Arg Ser Gly Pro Leu Thr Lys
            155                 160                 165
Asp Gly Glu Ile Glu Gly Gln Thr Ser Asn Ile Leu Ala Ser Gln
            170                 175                 180
Arg Arg Leu Ala Glu Ile Thr Glu Met Ile His Ala Ala Ser Leu
            185                 190                 195
Leu His Asp Asp Val Ile Asp Ala Ser Glu Thr Arg Arg Asn Ala
            200                 205                 210
Pro Ser Gly Asn Gln Ala Phe Gly Asn Lys Met Ala Ile Leu Ala
            215                 220                 225
```

```
Gly Asp Phe Leu Leu Gly Arg Ala Ser Val Ala Leu Ala Arg Leu
            230                 235                 240
Arg Asn Pro Glu Val Ile Glu Leu Leu Ala Thr Val Ile Ala Asn
            245                 250                 255
Leu Val Glu Gly Glu Phe Met Gln Leu Lys Asn Thr Val Asp Asp
            260                 265                 270
Ala Ile Glu Ala Thr Ala Thr Gln Glu Thr Phe Asp Tyr Tyr Leu
            275                 280                 285
Gln Lys Thr Tyr Leu Lys Thr Ala Ser Leu Ile Ala Lys Ser Cys
            290                 295                 300
Arg Ala Ser Ala Leu Leu Gly Gly Ala Thr Pro Glu Val Ala Asp
            305                 310                 315
Ala Ala Tyr Ala Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gln Ile
            320                 325                 330
Val Asp Asp Met Leu Asp Tyr Thr Val Ser Ala Thr Asp Leu Gly
            335                 340                 345
Lys Pro Ala Gly Ala Asp Leu Gln Leu Gly Leu Ala Thr Ala Pro
            350                 355                 360
Ala Leu Phe Ala Trp Lys His His Ala Glu Leu Gly Pro Met Ile
            365                 370                 375
Lys Arg Lys Phe Ser Asp Pro Gly Asp Val Glu Arg Ala Arg Glu
            380                 385                 390
Leu Val Glu Lys Ser Asp Gly Leu Glu Lys Thr Arg Ala Leu Ala
            395                 400                 405
Glu Glu Tyr Ala Gln Lys Ala Leu Asp Ala Ile Arg Thr Phe Pro
            410                 415                 420
Glu Ser Pro Ala Arg Lys Ala Leu Glu Gln Leu Thr Asp Lys Val
            425                 430                 435
Leu Thr Arg Ser Arg
            440
```

delete all underlines (global error)

~~<210> 3~~
~~<211> 24~~ ✓ ← *see item 11 on Error Summary Sheet*
~~<212> DNA~~ ✓
~~<213> Artificial Sequence~~

<400> 3 *see item 9 on Error Summary Sheet*

aaggatcct(n) yt(n)caygayg aygt   24

<210> 4
<211> 17
<212> DNA
<213> (Artificial Sequence) *item 11* *delete underlines*

<400> 4 *item 9*
aryt(n)adra ayt(n)cc   17

<210> 5
<211> 21
<212> DNA *item 11*
<213> (Artificial Sequence)

<400> 5 *delete underlines*

gagaccagac gaaacgcacc a   21

<210> 6
<211> 21

```
<212> DNA
<213> Artificial Sequence          item 11

<400> 6

tggtgcgttt cgtctggtct c          21      delete underlines

<210> 7
<211> 26
<212> DNA
<213> Artificial Sequence          item 11

<400> 7

aacatatggc ctcaccagca ctgcgg      26     delete underlines

<210> 8
<211> 29
<212> DNA
<213> Artificial Sequence          item 11

<400> 8                                   delete underlines

aagaattcct atcttgacct agtcaacac   29
```